RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/580,635
Source: IFW0
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RAW SEQUENCE LISTING DATE: 04/13/2007
PATENT APPLICATION: **US/10/580,635** TIME: 13:41:04

Input Set : **N:\EFS\04_13_07\10580635_efs\-500-1.txt**
Output Set: **N:\CRF4\04132007\J580635.raw**

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 3 <110> APPLICANT: Pastan, Ira H.
 4       Ho, Mitchell
 5       Bang, Sook-Hee
 6       The Government of the United States
 7       as represented by The Secretary of the
 8       Department of Health and Human Services
10 <120> TITLE OF INVENTION: Mutated Anti-CD22 Antibodies and Immunoconjugates
12 <130> FILE REFERENCE: 015280-500100US
14 <140> CURRENT APPLICATION NUMBER: US 10/580,635
15 <141> CURRENT FILING DATE: 2006-05-25
17 <150> PRIOR APPLICATION NUMBER: US 60/525,371
18 <151> PRIOR FILING DATE: 2003-11-25
20 <150> PRIOR APPLICATION NUMBER: WO PCT/US04/39617
21 <151> PRIOR FILING DATE: 2004-11-24
23 <160> NUMBER OF SEQ ID NOS: 30
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 321
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus sp.
32 <220> FEATURE:
33 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
34       antibody light chain variable region (VL)
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (1)..(321)
39 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
40       antibody light chain variable region (VL)
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44 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
45   1               5                  10                  15
47 gac aga gtc acc att agt tgc agg gca agt cag gac att agc aat tat   96
48 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
49              20                  25                  30
51 tta aac tgg tat cag cag aaa cca gat gga act gtt aaa ctc ctg atc   144
52 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
53          35                  40                  45
55 tac tac aca tca ata tta cac tca gga gtc cca tca agg ttc agt ggc   192
56 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
57      50                  55                  60
59 agt ggg tct gga aca gat tat tct ctc acc att agc aac ctg gag caa   240
60 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
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61  65                  70                  75                  80
63 gaa gat ttt gcc act tac ttt tgc caa cag ggt aat acg ctt ccg tgg   288
64 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
65                  85                  90                  95
67 acg ttc ggt gga ggc acc aag ctg gaa atc aaa                     321
68 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
69             100                 105
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 107
74 <212> TYPE: PRT
75 <213> ORGANISM: Mus sp.
77 <220> FEATURE:
78 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
79       antibody light chain variable region (VL)
81 <400> SEQUENCE: 2
82 Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
83   1               5                  10                  15
85 Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
86              20                  25                  30
88 Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
89          35                  40                  45
91 Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
92      50                  55                  60
94 Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
95  65                  70                  75                  80
97 Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
98                  85                  90                  95
100 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
101             100                 105
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 369
106 <212> TYPE: DNA
107 <213> ORGANISM: Mus sp.
109 <220> FEATURE:
110 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
111       antibody heavy chain variable region (VH)
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (1)..(369)
116 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
117       antibody heavy chain variable region (VH)
119 <400> SEQUENCE: 3
120 gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga ggg   48
121 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
122   1               5                  10                  15
124 tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc gct ttc agt atc tat   96
125 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
126              20                  25                  30
128 gac atg tct tgg gtt cgc cag act ccg gag aag agg ctg gag tgg gtc   144
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129 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
130          35                  40                  45
132 gca tac att agt agt ggt ggt ggt acc acc tac tat cca gac act gtg   192
133 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
134      50                  55                  60
136 aag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac   240
137 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
138  65                  70                  75                  80
140 ctg caa atg agc agt ctg aag tct gag gac aca gcc atg tat tac tgt   288
141 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
142                  85                  90                  95
144 gca aga cat agt ggc tac ggt agt agc tac ggg gtt ttg ttt gct tac   336
145 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
146              100                 105                 110
148 tgg ggc caa ggg act ctg gtc act gtc tct gca                      369
149 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
150          115                 120
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 123
155 <212> TYPE: PRT
156 <213> ORGANISM: Mus sp.
158 <220> FEATURE:
159 <223> OTHER INFORMATION: RFB4 mouse IgG1 anti-human CD22 monoclonal
160       antibody heavy chain variable region (VH)
162 <400> SEQUENCE: 4
163 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
164   1               5                  10                  15
166 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
167              20                  25                  30
169 Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
170          35                  40                  45
172 Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
173      50                  55                  60
175 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
176  65                  70                  75                  80
178 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
179                  85                  90                  95
181 Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
182              100                 105                 110
184 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
185          115                 120
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 4
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence:carboxyl
195       terminal fragment binding KDEL recycling receptor
196       for transport of construct into cytosol from
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Input Set : N:\EFS\04_13_07\10580635_efs\-500-1.txt
Output Set: N:\CRF4\04132007\J580635.raw

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197       endoplasmic reticulum
199 <400> SEQUENCE: 5
200 Lys Asp Glu Leu
201   1
204 <210> SEQ ID NO: 6
205 <211> LENGTH: 4
206 <212> TYPE: PRT
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Description of Artificial Sequence:carboxyl
211       terminal fragment binding KDEL recycling receptor
212       for transport of construct into cytosol from
213       endoplasmic reticulum
215 <400> SEQUENCE: 6
216 Arg Glu Asp Leu
217   1
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 6
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
227       light chain (VL) complementarity determining
228       region 1 (CDR1)
230 <400> SEQUENCE: 7
231 Gln Asp Ile His Gly Tyr
232   1               5
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 6
237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
242       light chain (VL) complementarity determining
243       region 1 (CDR1)
245 <400> SEQUENCE: 8
246 Gln Asp Ile Gly Arg Tyr
247   1               5
250 <210> SEQ ID NO: 9
251 <211> LENGTH: 6
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
257       light chain (VL) complementarity determining
258       region 1 (CDR1)
260 <400> SEQUENCE: 9
261 Gln Asp Ile Arg Gly Tyr
262   1               5
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Input Set : N:\EFS\04_13_07\10580635_efs\-500-1.txt
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265 <210> SEQ ID NO: 10
266 <211> LENGTH: 6
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
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273 region 1 (CDR1)
275 <400> SEQUENCE: 10
276 Gln Asp Ile Ala Arg Tyr
277 1 5
280 <210> SEQ ID NO: 11
281 <211> LENGTH: 3
282 <212> TYPE: PRT
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
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288 region 2 (CDR2)
290 <400> SEQUENCE: 11
291 Tyr Thr Ser
292 1
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 9
297 <212> TYPE: PRT
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
302 light chain (VL) complementarity determining
303 region 3 (CDR3)
305 <400> SEQUENCE: 12
306 Gln Gln Gly Asn Thr Leu Pro Trp Thr
307 1 5
310 <210> SEQ ID NO: 13
311 <211> LENGTH: 8
312 <212> TYPE: PRT
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence:RFB4 variable
317 heavy chain (VH) complementarity determining
318 region 1 (CDR1)
320 <400> SEQUENCE: 13
321 Gly Phe Ala Phe Ser Ile Tyr Asp
322 1 5
325 <210> SEQ ID NO: 14
326 <211> LENGTH: 8
327 <212> TYPE: PRT
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:

VERIFICATION SUMMARY DATE: 04/13/2007
PATENT APPLICATION: **US/10/580,635** TIME: 13:41:05

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